SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC. Kazusa DNA Research Institute

<120> Novel gene encoding brain-specific membrane protein

<130> C2-010PCT

<150> JP 1998-331727

<151> 1998-11-20

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<212> DNA

<213> Homo sapiens

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gccgggggta gatgctgcct cgcccaggcg ctgagtgacc agacc atg gag acc ctg 477 Met Glu Thr Leu

1

ctt ggt ggc ctg cta gcg ttt ggc atg gcg ttt gcc gtg gtc gac gcc 525 Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala 5 10 15 20

tgc ccc aag tac tgt gtc tgc cag aat ctg tct gag tca ctg ggg acc 573 Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr

25 30 35

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ctg tgc ccc tcc aag ggg ctg ctc ttt gta ccc cct gat att gac cgg Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg

621

40 45 50

cgg aca gtg gag ctg cgc ctg ggc ggc aac ttc atc atc cac atc agc 669 Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser 55 60 65

cgc cag gac ttt gcc aac atg acg ggg ctg gtg gac ctg acc ctg tcc 717 Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser 70 75 80

agg aac acc atc agc cac atc cag ccc ttt tcc ttt ctg gac ctc gag765Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu85909095100

agc ctc cgc tcc ctg cat ctt gac agc aat cgg ctg cca agc ctt ggg 813 Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly 105 110 115

gag gac acc ctc cgg ggc ctg gtc aac ctg cag cac ctt atc gtg aac 861 Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn 120 125 130

aac aac cag ctg ggc ggc atc gca gat gag gct ttt gag gac ttc ctg 909

Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu

135 140 145

ctg aca ttg gag gat ctg gac ctc tcc tac aac aac ctc cat ggc ctg957Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu150150155160

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ccg tgg gac tcc gtg cga cgc atg gtc aac ctc cac cag ctg agc ctg1005Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu165170175180

gac cac aac ctg ctg gat cac atc gcc gag ggc acc ttt gca gac ctg 1053 Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu 185 190 195

cag aaa ctg gcc cgc ctg gat ctc acc tcc aat cgg ctg cag aag ctg 1101 Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu

200 205 210

ccc cct gat ccc atc ttt gcc cgc tcc cag gct tcg gct ttg aca gcc 1149 Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala

215 220 225

aca ccc ttt gcc cca ccc ttg tcc ttt agt ttt ggg ggt aac cca ctt 1197 Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu

230 235 240

1245

245 250 255 260

His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp

- gac ctg gaa acc tgt ggc tcc cca ggg ggc ctc aag ggt cgc tac ttc 1293 Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe 265 270 275
- tgg cat gtg cgt gag gag gag ttt gtg tgc gag ccg cct ctc atc acc 1341 Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr 280 285 290
- cag cac aca cac aag ttg ctg gtt ctg gag ggc cag gcg gcc aca ctc 1389 Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu 295 300 305
- aag tgc aaa gcc att ggg gac ccc agc ccc ctt atc cac tgg gta gcc 1437 Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala

310 315 320

ccc gat gac cgc ctg gta ggg aac tcc tca agg acc gct gtc tat gac1485Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp325330335340

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345 350 355 ttc acc tgc att gct gcc aat gct gcc gga gag gcc acg gcc atg gtg 1581 Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val 360 365 370 gag gtc tcc atc gtc cag ctg cca cac ctc agc aac agc acc agc cgc 1629 Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg 375 380 385 act gca ccc ccc aag tcc cgc ctc tca gac atc act ggc tcc agc aag 1677

Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys390395400

acc agc cgg gga ggt gga ggc agt ggg ggc gga gag cct ccc aaa agc1725Thr Ser Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser410415420

ccc ccg gaa cgg gct gtg ctt gtg tct gaa gtg acc acc acc tcg gcc1773Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala425430435

ctg gtc aag tgg tct gtc agc aag tca gca ccc cgg gtg aag atg tac 1821 Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr

450

445

440

Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala

cag ctg cag tac aac tgc tct gac gat gag gta ctg att tac agg atg 1869 Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met

455 460 465

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act ggc tac gac ttg tgt gtg ctg gcc atg tgg gat gac aca gcc acg1965Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr485490495500

aca ctc acg gcc acc aac atc gtg ggc tgc gcc cag ttc ttc acc aag 2013 Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys 505 510 515

gct gac tac ccg cag tgc cag tcc atg cac agc cag att ctg ggc ggc 2061 Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly 520 525 530

acc atg atc ctg gtc atc ggg ggc atc atc gtg gcc acg ctg ctg gtc 2109 Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val

535 540 545

ttc atc gtc atc ctc atg gtg cgc tac aag gtc tgc aac cac gag gcc 2157

Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala

550 555

ccc agc aag atg gca gcg gcc gtg agc aat gtg tac tcg cag acc aac2205Pro Ser Lys Met Ala Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn565570575580

585 590 595

cag ggc ccg ccg aag gtg gtg gtg cgc aac gag ctc ctg gac ttc acc 2301 Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr 600 605 610

gcc agc ctg gcc cgc gcc agt gac tcc tct tcc tcc agc tcc ctg ggc 2349 Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly

615 620 625

agt ggg gag gct gcg ggg ctg gga cgg gcc ccc tgg agg atc cca ccc 2397 Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro

 630
 635
 640

tcc gcc ccg cgc ccc aag ccc agc ctt gac cgc ctg atg ggg gcc ttc2445Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe650655660

gcc tcc ctg gac ctc aag agt cag aga aag gag gag ctg ctg gac tcc 2493 Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser

665	670	675

agg act cca gcc ggg aga ggg gct ggg acg tcg gcc cgg ggc cac cac 2541 Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His 680 685 690

tcg gac cga gag cca ctg ctg ggg ccc cct gcg gcc cgg gcc agg agc 2589 Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser 695 700 705

ctg ctc ccc ttg ccg ttg gag ggc aag gcc aaa cgc agc cac tcc ttc 2637 Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe 710 715 720

ggc tac agt cct cct cgg aag gtc tcg aac atc tgg acg aag cgc agc 2733 Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser 745 750 755

ctc tct gtc aac ggc atg ctc ttg ccc ttt gag gag agt gac ctg gtg 2781

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Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val

760 765 770

ggg gcc cgg ggg act ttt ggc agc tcc gaa tgg gtg atg gag agc acg 2829 Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr

775 780 785

gtc taggtggggg tgggcatgct ccctttcctg tgcgcagggt gggagaaggg 2882 Val

gaaagaatet cactggcaag tgtttgtgga gtttccatgg tgatgtttac atccagggac 2942
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<211> 789

<212> PRT

<213> Homo sapiens

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													1		
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5		-			10					15				-	20
Cys	Pro	Lys	Tyr	Cys	Val	Cys	Gln	Asn	Leu	Ser	Glu	Ser	Leu	Gly	Thr
				25					30					35	
Leu	Cys	Pro	Ser	Lys	Gly	Leu	Leu	Phe	Val	Pro	Pro	Asp	Ile	Asp	Arg
			40					45					50		
Arg	Thr	Val	Glu	Leu	Arg	Leu	Gly	Gly	Asn	Phe	Ile	Ile	His	Ile	Ser
		55					60					65			
	01					1	m 1						m 1		•
Arg		Asp	Pne	Ala	Asn		Inr	GIY	Leu	Val		Leu	Inr	Leu	Ser
	70					75					80				
Arg	Asn	Thr	Ile	Ser	His	Ile	Gln	Pro	Phe	Ser	Phe	Leu	Asp	Leu	Glu
85					90					95			•		100
Ser	Leu	Arg	Ser	Leu	His	Leu	Asp	Ser	Asn	Arg	Leu	Pro	Ser	Leu	Gly
				105					110					115	

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120 125 130 Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu 135 140 145 Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu 150 155 160 Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu 170 175 180 165 Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu 185 190 195 Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu 200 205 210 Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala 215 220 225 Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu 230 235 240 His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp

245 250 255 260

Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn

Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg

Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys

Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly

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	Phe	1
		58
	Pro	Se
	565	
anna cana cana a	Gly	A
anna - a anna a anna anna anna anna ann	Gln	G]
n dagt fan ster under t	Ala	Se

le Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala er Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn la Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro ly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr er Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe

Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser

665 670 675

Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val

Arg	Thr	Pro	Ala	Gly	Arg	Gly	Ala	Gly	Thr	Ser	Ala	Arg	Gly	His	His
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Ser	Asp	Arg	Glu	Pro	Leu	Leu	Gly	Pro	Pro	Ala	Ala	Arg	Ala	Arg	Ser
		695					700					705			
Leu	Leu	Pro	Leu	Pro,	Leu	Glu	Gly	Lys	Ala	Lys	Arg	Ser	His	Ser	Phe
	710					715					720				
Asp	Met	Gly	Asp	Phe	Ala	Ala	Ala	Ala	Ala	Gly	Gly	Val	Val	Pro	Gly
725					730					735					740
Gly	Tyr	Ser	Pro		Arg	Lys	Val	Ser	Asn	Ile	Trp	Thr	Lys	Arg	Ser
				745					750					755	
Leu	Ser	Val		Gly	Met	Leu	Leu		Phe	Glu	Glu	Ser	Asp	Leu	Val
			760					765					770		
				(1)		a 1	-	-		_					
Gly	Ala		Gly	Thr	Phe	Gly		Ser	Glu	Trp	Val		Glu	Ser	Thr
		775					780					785			

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16/19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an

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<210> 4

<211> 16

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an

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<210> 5

<211> 12

<212> DNA

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<220>

<223> Description of Artificial Sequence: an

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<210> 6

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an

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<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: an

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<400> 7

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